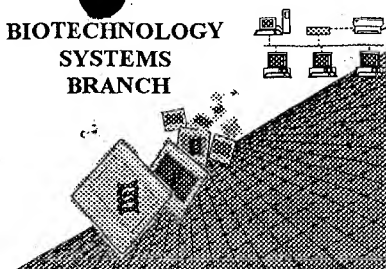


WTH

BIOTECHNOLOGY  
SYSTEMS  
BRANCH



0400  
05-01-01.

## RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/823,649  
Source: OIP  
Date Processed by STIC: 4/20/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

### Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST 25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

# Raw Sequence Listing Error Summary

## ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/823,649

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 \_\_\_\_\_ Wrapped Nucleics      The number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 \_\_\_\_\_ Wrapped Aminos      The amino acid number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 \_\_\_\_\_ Incorrect Line Length      The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 \_\_\_\_\_ Misaligned Amino Acid      The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs  
Numbering      between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 \_\_\_\_\_ Non-ASCII      This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.  
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 \_\_\_\_\_ Variable Length      Sequence(s) \_\_\_\_\_ contain n's or Xaa's which represented more than one residue.  
As per the rules, each n or Xaa can only represent a single residue.  
Please present the maximum number of each residue having variable length and  
indicate in the (ix) feature section that some may be missing.
- 7 \_\_\_\_\_ PatentIn ver. 2.0 "bug"      A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid  
sequence(s) \_\_\_\_\_. Normally, PatentIn would automatically generate this section from the  
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section  
to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223>  
sections for Artificial or Unknown sequences.
- 8 \_\_\_\_\_ Skipped Sequences      Sequence(s) \_\_\_\_\_ missing. If intentional, please use the following format for each skipped sequence:  
(OLD RULES)      (2) INFORMATION FOR SEQ ID NO:X:  
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")  
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:  
This sequence is intentionally skipped  
  
Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 \_\_\_\_\_ Skipped Sequences      Sequence(s) \_\_\_\_\_ missing. If intentional, please use the following format for each skipped sequence.  
(NEW RULES)      <210> sequence id number  
<400> sequence id number  
000
- 10 \_\_\_\_\_ Use of n's or Xaa's      Use of n's and/or Xaa's have been detected in the Sequence Listing.  
(NEW RULES)      Use of <220> to <223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 \_\_\_\_\_ Use of "Artificial"      Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules.  
(NEW RULES)      Valid response is Artificial Sequence.
- 12 \_\_\_\_\_ Use of <220>Feature      Sequence(s) \_\_\_\_\_ are missing the <220>Feature and associated headings.  
(NEW RULES)      Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial Sequence" or "Unknown"  
Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 \_\_\_\_\_ PatentIn ver. 2.0 "bug"      Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted  
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).  
Instead, please use "File Manager" or any other means to copy file to floppy disk.

OIPE

## RAW SEQUENCE LISTING

DATE: 04/20/2001

PATENT APPLICATION: US/09/823,649

TIME: 07:42:37

Input Set : A:\RPA1006.ST25.txt

Output Set: N:\CRF3\04202001\I823649.raw

Does Not Comply  
Corrected Diskette Needed

pg 1-3,5

3 <110> APPLICANT: Smith, Edward  
 4 Elfstrom, Carita  
 5 Gelfand, David  
 6 Higuchi, Russell  
 7 Myers, Thomas  
 8 Schoenbrunner, Nancy  
 9 Wang, Alice  
 11 <120> TITLE OF INVENTION: HIGH TEMPERATURE REVERSE TRANSCRIPTION USING MUTANT DNA POLYMERASES  
 13 <130> FILE REFERENCE: RPA1006  
 C--> 15 <140> CURRENT APPLICATION NUMBER: US/09/823,649  
 C--> 15 <141> CURRENT FILING DATE: 2001-03-30  
 15 <150> PRIOR APPLICATION NUMBER: US 60/198,336  
 16 <151> PRIOR FILING DATE: 2000-04-18  
 18 <160> NUMBER OF SEQ ID NOS: 21  
 20 <170> SOFTWARE: PatentIn version 3.0  
 22 <210> SEQ ID NO: 1  
 23 <211> LENGTH: 11  
 24 <212> TYPE: PRT  
 C--> 25 <213> ORGANISM: Artificial *see item 11 on Encl Summary Sheet*  
 27 <220> FEATURE:  
 28 <223> OTHER INFORMATION: sequence motif  
 30 <220> FEATURE:  
 31 <221> NAME/KEY: VARIANT  
 32 <222> LOCATION: (2)..(2)  
 33 <223> OTHER INFORMATION: X is S or A  
 36 <220> FEATURE:  
 37 <221> NAME/KEY: VARIANT  
 38 <222> LOCATION: (3)..(3)  
 39 <223> OTHER INFORMATION: X is any amino acid  
 42 <220> FEATURE:  
 43 <221> NAME/KEY: VARIANT  
 44 <222> LOCATION: (4)..(4)  
 45 <223> OTHER INFORMATION: X is any amino acid  
 48 <220> FEATURE:  
 49 <221> NAME/KEY: VARIANT  
 50 <222> LOCATION: (5)..(5)  
 51 <223> OTHER INFORMATION: X is L or I  
 54 <220> FEATURE:  
 55 <221> NAME/KEY: VARIANT  
 56 <222> LOCATION: (6)..(6)  
 57 <223> OTHER INFORMATION: X is any amino acid  
 60 <220> FEATURE:  
 61 <221> NAME/KEY: VARIANT  
 62 <222> LOCATION: (7)..(7)  
 63 <223> OTHER INFORMATION: X is any amino acid  
 66 <220> FEATURE:  
 67 <221> NAME/KEY: VARIANT

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/823,649

DATE: 04/20/2001  
TIME: 07:42:37

Input Set : A:\RPA1006.ST25.txt  
Output Set: N:\CRF3\04202001\I823649.raw

68 <222> LOCATION: (8)..(8)  
69 <223> OTHER INFORMATION: X is any amino acid  
72 <220> FEATURE:  
73 <221> NAME/KEY: VARIANT  
74 <222> LOCATION: (9)..(9)  
75 <223> OTHER INFORMATION: X is any amino acid  
78 <220> FEATURE:  
79 <221> NAME/KEY: VARIANT  
80 <222> LOCATION: (10)..(10)  
81 <223> OTHER INFORMATION: X is any amino acid  
OK 84 <400> SEQUENCE: 1  
86 Leu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Glu  
87 1 5 10  
89 <210> SEQ ID NO: 2  
90 <211> LENGTH: 11  
91 <212> TYPE: PRT  
C--> 92 <213> ORGANISM: Artificial *item 11*  
94 <220> FEATURE:  
95 <223> OTHER INFORMATION: sequence motif  
97 <220> FEATURE:  
98 <221> NAME/KEY: VARIANT  
99 <222> LOCATION: (3)..(3)  
100 <223> OTHER INFORMATION: X is Q or G  
103 <220> FEATURE:  
104 <221> NAME/KEY: VARIANT  
105 <222> LOCATION: (6)..(6)  
106 <223> OTHER INFORMATION: X is S or A  
OK 109 <400> SEQUENCE: 2  
111 Leu Ser Xaa Glu Leu Xaa Ile Pro Tyr Glu Glu  
112 1 5 10  
114 <210> SEQ ID NO: 3  
115 <211> LENGTH: 11  
116 <212> TYPE: PRT  
C--> 117 <213> ORGANISM: Artificial  
119 <220> FEATURE:  
120 <223> OTHER INFORMATION: sequence motif  
122 <400> SEQUENCE: 3  
124 Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu Glu  
125 1 5 10  
127 <210> SEQ ID NO: 4  
128 <211> LENGTH: 11  
129 <212> TYPE: PRT  
C--> 130 <213> ORGANISM: Artificial  
132 <220> FEATURE:  
133 <223> OTHER INFORMATION: sequence motif  
135 <220> FEATURE:  
136 <221> NAME/KEY: VARIANT  
137 <222> LOCATION: (3)..(3)  
138 <223> OTHER INFORMATION: X is Q or G

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/823,649

DATE: 04/20/2001  
TIME: 07:42:37

Input Set : A:\RPA1006.ST25.txt  
Output Set: N:\CRF3\04202001\I823649.raw

141 <400> SEQUENCE: 4  
143 Leu Ser Xaa Glu Leu Ser Ile Pro Tyr Glu Glu  
144 1 5 10  
146 <210> SEQ ID NO: 5  
147 <211> LENGTH: 11  
148 <212> TYPE: PRT  
C--> 149 <213> ORGANISM: Artificial  
151 <220> FEATURE:  
152 <223> OTHER INFORMATION: sequence motif  
154 <220> FEATURE:  
155 <221> NAME/KEY: VARIANT  
156 <222> LOCATION: (7)..(7)  
157 <223> OTHER INFORMATION: X is V or I  
160 <400> SEQUENCE: 5  
162 Leu Ser Val Arg Leu Gly Xaa Pro Val Lys Glu  
163 1 5 10  
165 <210> SEQ ID NO: 6  
166 <211> LENGTH: 11  
167 <212> TYPE: PRT  
C--> 168 <213> ORGANISM: Artificial  
170 <220> FEATURE:  
171 <223> OTHER INFORMATION: sequence motif  
173 <400> SEQUENCE: 6  
175 Leu Ser Lys Arg Ile Gly Leu Ser Val Ser Glu  
176 1 5 10  
178 <210> SEQ ID NO: 7  
179 <211> LENGTH: 11  
180 <212> TYPE: PRT  
C--> 181 <213> ORGANISM: Artificial  
183 <220> FEATURE:  
184 <223> OTHER INFORMATION: sequence motif  
186 <220> FEATURE:  
187 <221> NAME/KEY: VARIANT  
188 <222> LOCATION: (8)..(8)  
189 <223> OTHER INFORMATION: X is S or T  
192 <400> SEQUENCE: 7  
194 Leu Ala Gln Asn Leu Asn Ile Xaa Arg Lys Glu  
195 1 5 10  
197 <210> SEQ ID NO: 8  
198 <211> LENGTH: 11  
199 <212> TYPE: PRT  
200 <213> ORGANISM: Thermus aquaticus  
202 <400> SEQUENCE: 8  
204 Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu Glu  
205 1 5 10  
207 <210> SEQ ID NO: 9  
208 <211> LENGTH: 11  
209 <212> TYPE: PRT  
210 <213> ORGANISM: Thermus flavus